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Set     Items   Description
S1   11252768   TEMPLAT? OR FORM OR FORMS OR FORMAT? OR CHART? OR GRAPH? OR
             PATTERN?
S2    5029895   DNA OR RNA OR CDNA OR MRNA OR (NUCLEOTIDE? OR BASE OR GENE-
            TIC? OR AMINO()ACID? OR PROTEIN? OR GENE)()SEQUENC?
S3    1076324   PROBE? OR PROBEARRAY?
S4    1618515   IDENTIFIER? OR ID OR DATA()STRUCTUR? OR LABEL? OR TAG OR T-
            AGGED OR TAGGING OR TAGS OR FLAGS OR FLAGGING OR FLAGGED
S5    3705019   RADIOACTIV? OR ISOTOP? OR ION? ?
S6    1101457   DATABASE? OR DATABANK? OR DATAMIN? OR DATA()(BASE? OR BANK?
            OR MINE? OR MINING OR VALUE?) OR DB OR RDB? OR DBMS? OR OODB?
S7      74678   S1 AND S2 AND S3
S8        156   S1 AND S2 AND S4 AND S5 AND S6
S9         24   S7 AND S8
S10         0   S1(5N)S3 AND S9
S11         0   S1(3N)S3 AND S8
S12        97   S2(2N)S3 AND S1 AND S4 AND S6
S13       110   S9 OR S12
S14        31   S8 AND (MANAGE? OR ADMINIST? OR CONTROL?)
S15       137   S13 OR S14
S16        84   RD (unique items)
S17        58   S16 NOT PY>2001
S18        54   S17 NOT PD>20010719
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01152610 ORDER NO: AAD91-11031

GENES EXPRESSED DURING OOGENESIS IN CALLIPHORA ERYTHROCEPHALA AND DROSOPHILA MELANOGASTER

Author: DE VALOIR, TAMSEN VIVIANNE

Degree: PH.D.
Year: 1990
Corporate Source/Institution: RICE UNIVERSITY (0187)
Adviser: K. BECKINGHAM
Source: VOLUME 51/11-B OF DISSERTATION ABSTRACTS INTERNATIONAL.
PAGE 5156. 153 PAGES
Descriptors: BIOLOGY, MOLECULAR; BIOLOGY, ENTOMOLOGY; BIOLOGY, GENETICS
Descriptor Codes: 0307; 0353; 0369

We were interested in identifying genes in the dipteran flies Calliphora erythrocephala and Drosophila melanogaster with a role in oogenesis and early embryogenesis. A biochemical screen was used to complement the extensive genetic screens that have been performed to identify such genes in Drosophila. Radio- **labelled cDNA probes** were made using poly(A)$\sp+$ RNA preparations from staged Calliphora ovaries and embryos. These probes were used to isolate clones which were strongly expressed during oogenesis but not during embryogenesis.

Four Calliphora genes which are absolutely "oogenesis-specific" in their expression **pattern** , as defined by our screening protocol, were identified. These are called A10B, B8I, C7F and GG7K. Three of these clones are expressed in the somatically derived follicle cells of the ovary and have been identified as being homologous to the Drosophila yolk protein 1 (A10B and B8I) and a vitelline membrane protein (GG7K). Interestingly, the yolk protein homologs are expressed in a specialized subset of follicle cells known as the border cells in Calliphora. The fourth gene, (C7F) is expressed in the nurse cells, the transcripts are translocated to the oocyte proper and maintained throughout the first four hours of embryogenesis. C7F is also expressed in late pupae and adult male flies.

A number of Calliphora genes were identified which, although not oogenesis-specific, were more strongly expressed in the oocyte than the embryo. These were classified as "oogenesis-differentials". C7F and the Calliphora oogenesis-differential genes were used to screen Drosophila cDNA and genomic libraries for homologs. Some characterization of these Drosophila homologs is described here.

ME31B, a maternally expressed Drosophila gene from the 31B region of the second chromosome was isolated by directly screening Drosophila libraries with Calliphora **cDNA probes** . ME31B is expressed throughout oogenesis and the transcript is maintained in the mature egg until four hours after fertilization. The ME31B transcript is evenly distributed throughout the oocyte and egg.

A 1.5 kb cDNA for ME31B was completely sequenced. Comparison of the coding sequence with a protein **data bank** allowed us to show that ME31B is a member of a family of NTP-dependent helicases. The possible mutant phenotype of ME31B is discussed.

18/5/5 (Item 2 from file: 144)
DIALOG(R)File 144:Pascal
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14674300 PASCAL No.: 00-0347724

Comprehensive gene expression profile of the adult human renal cortex : Analysis by cDNA array hybridization

YANO N; ENDOH M; FADDEN K; YAMASHITA H; KANE A; SAKAI H; RIFAI A
Department of Pathology, Rhode Island Hospital and Brown University School of Medicine, Providence, Rhode Island, United States; Division of Nephrology and Metabolism, Department of Internal Medicine, Tokai University School of Medicine, Kanagawa, Japan

Journal: Kidney international, 2000, 57 (4) 1452-1459
ISSN: 0085-2538 CODEN: KDYIA5 Availability: INIST-15906; 354000082190090330
No. of Refs.: 19 ref.
Document Type: P (Serial) ; A (Analytic)
Country of Publication: United States
Language: English

Background. Profiling of gene expression in healthy and diseased renal tissue is important for elucidating the pathogenesis of renal diseases. Comprehensive information about the genes expressed in renal tissue is unavailable. The recently developed **cDNA** array hybridization methodology allows simultaneous monitoring of thousands of genes expressed renal tissue. Methods. Complex (alpha - SUP 3 SUP 3 P)- **labeled cDNA probes** were prepared from histopathologically uninvolved remnants of nine renal tissues obtained by nephrectomy. Each **probe** was hybridized to a high-density array of 18,326 paired target genes. The **radioactive** hybridization signals by phosphorimager screens were quantitated by special software. Bioinformatics from public genomic **databases** were used to assign a chromosomal location of each expressed transcript and gene function. Cluster analysis was used to arrange genes according to the similarity in **pattern** of gene expression. Results, A total of 7563 different gene transcripts was detected in the nine tissue samples. Approximately 870 of these genes were full-length **mRNA** human transcripts (HT), and the remaining 6693 were expressed sequence **tags** (ESTs). The full-length transcripts were classified by function of the gene product and were listed with information of their chromosomal positions. To allow a comparison between gene expression in clinical and experimental studies, the mouse genes with known similar function to the human counterpart were included in the bioinformatics analysis. Cluster analysis of 502 full-length genes that are expressed in four or more renal tissues revealed more than 110 genes that are highly expressed in all the renal specimens. Conclusions. The presented data constitute a comprehensive preliminary transcriptional map of the adult human renal cortex. The information may serve as a resource for speeding up the discovery of genes underlying human renal disease. The integrated listing of the full-length expressed human and mouse genes is available through e-mail (AbdallaRifai@Brown.edu).

English Descriptors: Renal cortex; Kidney; Transcription; **RNA** ; **DNA** ; Genetic determinism; Human
Broad Descriptors: Urinary system; Appareil urinaire; Aparato urinario

French Descriptors: Corticale renale; Rein; Transcription; **RNA** ; **DNA** ;

18/5/12 (Item 3 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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07528183 Genuine Article#: 176KD Number of References: 19
Title: Expression profiling in cancer using cDNA microarrays
Author(s): Khan J; Saal LH; Bittner ML; Chen YD; Trent JM; Meltzer PS (REPRINT)
Corporate Source: NATL HUMAN GENOME RES INST,CANC GENET BRANCH, NIH, BLDG 49, ROOM 4A10, 49 CONVENT DR/BETHESDA//MD/20892 (REPRINT); NATL HUMAN GENOME RES INST,CANC GENET BRANCH, NIH/BETHESDA//MD/20892
Journal: ELECTROPHORESIS, 1999, V20, N2 (FEB), P223-229
ISSN: 0173-0835 Publication date: 19990200
Publisher: WILEY-V C H VERLAG GMBH, MUHLENSTRASSE 33-34, D-13187 BERLIN, GERMANY
Language: English Document Type: REVIEW
Geographic Location: USA
Subfile: CC LIFE--Current Contents, Life Sciences
Journal Subject Category: BIOCHEMICAL RESEARCH METHODS; CHEMISTRY, ANALYTICAL
Abstract: Currently there are over 1 000 000 human expressed sequence **tag** (EST) sequences available on the public **database** , representing perhaps 50-90% of all human genes. The cDNA microarray technique is a recently developed tool that exploits this wealth of information for the analysis of gene expression. In this method, **DNA probes** representing **cDNA** clones are arrayed onto a glass slide and interrogated with fluorescently **labeled** cDNA targets. The power: of the technology is the ability to perform a genome-wide expression profile of thousands of genes in one experiment. In our review we describe the principles of the microarray technology as applied to cancer research, summarize the literature on its use so far, and speculate on the future application of this powerful technique.
Descriptors--Author Keywords: cDNA microarray ; gene expression ; cancer research ; review
Identifiers--KeyWord Plus(R): GENE-EXPRESSION; HUMAN GENOME; DNA MICROARRAY; HYBRIDIZATION; **PATTERNS;** MAP
Cited References:
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18/5/14 (Item 5 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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06109969 Genuine Article#: XV699 Number of References: 22
Title: Purification and cloning of a proline 3-hydroxylase, a novel enzyme which hydroxylates free L-proline to cis-3-hydroxy-L-proline
Author(s): Mori H; Shibasaki T; Yano K; Ozaki A (REPRINT)
Corporate Source: KYOWA HAKKO KOGYO CO LTD,TOKYO RES LABS, 3-6-6 ASAHIMACHI/MACHIDA/TOKYO 194/JAPAN/ (REPRINT); KYOWA HAKKO KOGYO CO LTD,TOKYO RES LABS/MACHIDA/TOKYO 194/JAPAN/
Journal: JOURNAL OF BACTERIOLOGY, 1997, V179, N18 (SEP), P5677-5683
ISSN: 0021-9193 Publication date: 19970900
Publisher: AMER SOC MICROBIOLOGY, 1325 MASSACHUSETTS AVENUE, NW, WASHINGTON, DC 20005-4171
Language: English Document Type: ARTICLE
Geographic Location: JAPAN
Subfile: CC LIFE--Current Contents, Life Sciences
Journal Subject Category: MICROBIOLOGY
Abstract: Proline 3-hydroxylase was purified from Streptomyces sp, strain TH1, and its structural gene was cloned, The purified enzyme hydroxylated free L-proline to cis-3-hydroxy-L-proline and showed properties of a 2-oxoglutarate-dependent dioxygenase (H, Mori, T, Shibasaki, Y, Uosaki, K. Ochiai, and A, Ozaki, Appl, Environ, Microbiol. 62:1903-1907, 1996), The molecular mass of the purified enzyme was 35 kDa as determined by sodium dodecyl sulfate-polyacrylamide gel electrophoresis, The isoelectric point of the enzyme was 4.3. The optimal pH and temperature were 7.0 and 35 degrees C, respectively, The K-m values were 0.56 and O.11 mM for L-proline and 2-oxoglutarate, respectively, The k(cat) value of hydroxylation was 3.2 s(-1). Determined N-terminal and internal amino acid sequences of the purified protein were not found in the SwissProt protein **database** , A DNA fragment of 74 bp was amplified by PCR with degenerate primers based on the determined N-terminal amino acid sequence, With this fragment as a **template** , a digoxigenin- **labeled** N-terminal probe was synthesized by PCR, A 6.5-kbp chromosome fragment was cloned by colony hybridization with the **labeled probe** , The determined **DNA** sequence of the cloned fragment revealed a 870-bp open reading frame (ORF 3), encoding a protein of 290 amino acids with a calculated molecular weight of 33,158, No sequence homolog was found in EMBL, GenBank, and DDBJ **databases** , ORF 3 was expressed in Escherichia coli DH1, Recombinants showed hydroxylating activity five times higher than that of the original bacterium, Streptomyces sp, strain TH1, It was concluded that the ORF 3 encodes functional proline 3-hydroxylase.
Identifiers--KeyWord Plus(R): STREPTOMYCES; PROTEINS; 4-HYDROXYLASE; BIOSYNTHESIS; QUANTITIES; MECHANISM; SEQUENCE
Research Fronts: 95-3190 002 (INCREASED ABUNDANCE OF SPECIFIC SKELETAL-MUSCLE PROTEIN-TYROSINE PHOSPHATASES; ALPHA-B-CRYSTALLIN EXPRESSION)
95-5061 002 (STRUCTURAL GENE; GLTC-DEPENDENT REGULATION OF BACILLUS-SUBTILIS GLUTAMATE SYNTHASE EXPRESSION; ARABIDOPSIS TYPE-1 PROTEIN PHOSPHATASE)
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18/5/15 (Item 6 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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04912456 Genuine Article#: UR281 Number of References: 21
Title: SEQUENCE PATTERNS **PRODUCED BY INCOMPLETE ENZYMATIC DIGESTION OR ONE-STEP EDMAN DEGRADATION OF PEPTIDE MIXTURES AS** PROBES **FOR PROTEIN** DATABASE **SEARCHES**
Author(s): JENSEN ON; VORM O; MANN M
Corporate Source: EUROPEAN MOLEC BIOL LAB,MEYERHOFSTR 1/D-69012 HEIDELBERG//GERMANY/; EUROPEAN MOLEC BIOL LAB/D-69012 HEIDELBERG//GERMANY/
Journal: ELECTROPHORESIS, 1996, V17, N5 (MAY), P938-944
ISSN: 0173-0835
Language: ENGLISH Document Type: ARTICLE
Geographic Location: GERMANY
Subfile: SciSearch; CC LIFE--Current Contents, Life Sciences
Journal Subject Category: BIOMETHODS
Abstract: Mass spectrometric peptide mapping of proteins isolated by polyacrylamide gel electrophoresis is a rapid method for identifying proteins in sequence **databases** . A majority of tryptic peptide maps were found to contain pairs of peptide **ion** peaks separated by the molecular weight of the lysyl or arginyl residue. These peaks originate from **amino acid sequence patterns** such as Lys-Lys where trypsin has cleaved C-terminals to either one of the lysines. The peptide mass and the **pattern** define an N- or C-terminal sequence **tag** . Searching sequence **databases** by such a sequence **tag** results in only a moderate number of matches and significantly reduces the number of **database** matches when used in combination with a peptide mass map. Two N- or C-terminal sequence **tags** alone unambiguously identify a protein in most cases. The technique discussed here is simple, does not require additional measurements, and increases the percentage of protein samples that can be identified by their mass maps alone. N-Terminal peptide sequence **tags** for **database** searching can also be generated by manual one-step Edman degradation of the unseparated peptide mixture.
Descriptors--Author Keywords: MATRIX-ASSISTED LASER DESORPTION IONIZATION ; **DATABASE** SEARCHING ; MASS SPECTROMETRY ; PEPTIDE SEQUENCING ; PROTEIN IDENTIFICATION
Identifiers--KeyWords Plus: IDENTIFICATION
Cited References:
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18/5/24 (Item 15 from file: 34)
DIALOG(R)File 34:SciSearch(R) Cited Ref Sci
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02135807 Genuine Article#: KD642 Number of References: 11
Title: A COMPARISON OF MODELS USED FOR CALCULATION OF RFLP PATTERN FREQUENCIES
Author(s): HERRIN G
Corporate Source: GEORGIA BUR INVESTIGAT,DIV FORENS SCI/DECATUR//GA/00000
Journal: JOURNAL OF FORENSIC SCIENCES, 1992, V37, N6 (NOV), P1640-1651
ISSN: 0022-1198
Language: ENGLISH Document Type: NOTE
Geographic Location: USA
Subfile: SciSearch; CC CLIN--Current Contents, Clinical Medicine
Abstract: In recent years the application of DNA typing information to criminal investigations has gained widespread acceptance. The primary method currently in use relies on length variation of DNA restriction fragments between individuals. These variations are identified using variable number tandem repeat (VNTR) **DNA probes** . As this technology becomes more widely used, it is crucial that scientifically valid methods of interpreting the significance of a DNA typing result be adopted. The method chosen should not only give a reliable approximation of the statistical likelihood of a particular RFLP **pattern** occurring, but should also be easy to present and for the court to understand. In this manuscript five methods of calculating a frequency of occurrence of a RFLP **pattern** will be presented (fixed bin genotype, floating bin phenotype, floating bin genotype, National Research Council (NRC) method using fixed bins and the NRC method using floating bins). The calculations discussed here demonstrated that the fixed bin genotype method produces a frequency very similar to that obtained from floating bin phenotypes. In addition, regardless of the method chosen or the **database** size, the frequency of any particular banding **pattern** in the population over several loci was found to be very rare.
Descriptors--Author Keywords: CRIMINALISTICS ; RFLP STATISTICS ; DNA TYPING
Identifiers--KeyWords Plus: LOCI
Research Fronts: 91-0567 002 (DNA FINGERPRINTING; P-32 **LABELED** OLIGONUCLEOTIDE PROBES; MULTIPLE PATERNITY IN WILD COMMON SHREWS (SOREX-ARANEUS))
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